IN THE SPECIFICATION

Please replace the paragraph beginning on page 5, line 16 with the following:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) (available on the worldwide web at ~~http://www.~~ddbj.nig.ac.jp/); Genebank (available on the worldwide web at the NCBI website at ~~http://www.ncbi.nlm.nih.gov~~/web/Genbank/Index.html): and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (available on the worldwide web at ~~http://www.~~ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequence queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12: 76-80 (1994); Birren, *et al., Genome Analysis,* 1: 543-559 (1997)).

Please replace the paragraph beginning on page 28, line 16 with the following:

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (available on the worldwide web at [[www-]]genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (available on the worldwide web at: [[www-]]genome.wi.mit.edu/cgi-bin/www-

STS_Pipeline), or GeneUp (Pesole, *et al.*, *Biotechniques* 25: 112-123 (1998) the entirety

of which is incorporated herein by reference), for example, can be used to identify

potential PCR primers.